

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 8, 2001, 16:29:17 ; Search time 13.59 Seconds

(without alignments)
190.577 Million cell updates/sec

Title: US-09-447-800-1

Perfect score: 176

Sequence: 1 XVEIQLMHNIGKHLMSREWEVLRRKLDQVHNF 34

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.68:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	100.0	115	1	PTHU
2	168	95.5	115	1	PTHU
3	167	94.9	115	1	PTHU
4	167	94.9	115	2	JC4202
5	158	89.8	115	2	A05091
6	150	85.2	105	2	I51851
7	121	68.8	119	2	A34937
8	61	34.7	824	2	F72408
9	58	33.0	175	1	JN0103
10	58	33.0	177	1	PTHU2L
11	58	33.0	177	1	A30012
12	58	33.0	177	2	JC4201
13	58	33.0	209	1	PTHU3L
14	56	31.8	115	2	H72705
15	55	31.2	94	2	T09450
16	55	31.2	94	2	C64559
17	54	30.7	176	1	SI0202
18	54	30.7	564	2	T38291
19	54	30.7	564	2	T43298
20	54	30.7	1257	1	I58383
21	54	30.7	2470	2	S57085
22	52	29.5	363	2	F70195
23	51.5	29.3	508	1	A43713
24	51.5	29.3	528	2	D65214
25	51.5	29.3	528	2	C86099
26	51.5	29.3	560	2	C41539
27	51.5	29.3	560	2	I53013
28	51	29.0	336	2	F84056
29	51	29.0	611	2	S38162

nucleotides

30	51	29.0	752	1	C2HU	complement C2 prec
31	51	29.0	764	1	BBHU	complement factor
32	51	29.0	1038	2	T15098	hypothetical prote
33	51	29.0	2182	2	T14320	calcineurin inhibi
34	51	29.0	2479	1	MNWVRA	nonstructural inhibi
35	50.5	28.7	145	2	EN4938	flagellar flid pro
36	50.5	28.7	3394	2	T18501	hypothetical prote
37	50	28.4	91	1	C64069	virulence-associat
38	50	28.4	570	2	G72595	hypothetical prote
39	50	28.4	722	2	B65583	transcription elon
40	50	28.4	722	2	C72040	transcription elon
41	50	28.4	2473	1	S38040	1-phosphatidylinos
42	50	28.4	3678	2	S28916	dystrophin - mouse
43	49.5	28.1	339	2	T18926	hypothetical prote
44	49.5	28.1	490	1	S71776	calcium-dependent
45	49.5	28.1	564	1	HMTWC2	hemagglutinin prec

ALIGNMENTS

RESULT 1

PTHU

parathyroid hormone precursor [validated] - human

N:Alternate names: proparathyroid hormone

C:Species: Homo sapiens (man)

C:Date: 24-Apr-1984 #sequence-revision 19-Jan-1996 #text-change 08-Dec-2000

C:Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94410;

R:Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Potts Jr.

Proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983

A:Title: Nucleotide sequence of the human parathyroid hormone gene.

A:Reference number: A19339; MUID:83169834

A:Accession: A19339

A:Molecule type: DNA

A:Residues: 1-115 <VAS>

A:Cross-references: GB:J00301; NID:G190702; PIDN:AAA60215.1; PID:G190704

R:Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.

Biol. Chem. Hoppe-Seyler 375, 821-824, 1994

A:Title: Purification of meprin from human kidney and its role in parathyroid hormone

A:Reference number: S53790; MUID:95225988

A:Accession: S53790

A:Molecule type: Protein

A:Residues: 'X', '33', 'X', '35-46;65-84;105-110 <YAM>

A>Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also occu

R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.

Nature 249, 155-157, 1974

A:Title: Structural analysis of human proparathyroid hormone by a new microsequencing

A:Reference number: A93169; MUID:74174967

A:Accession: A93169

A:Molecule type: protein

A:Residues: 26-37 <JAC>

R:Olstead, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gautvik,

Eur. J. Biochem. 205, 311-319, 1992

A:Title: Isolation and characterization of two biologically active O-glycosylated for

ation.

A:Reference number: S21199; MUID:92209518

A:Accession: S21199

A:Molecule type: Protein

A:Residues: 32-114, 'N' <OLS>

A>Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosylati

R:Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan, J.L

Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974

A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parathyro

A:Reference number: A93789; MUID:74111656

A:Accession: A93789

A:Molecule type: protein

A:Residues: 32-68 <NIA>

R:Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.

Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A:Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal residue

A:Reference number: A93783; MUID:73070429

A:Accession: A93783

A:Molecule type: protein

C:Species: Canis lupus familiaris (dog)
C:Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 16-Jul-1999
C:Accession: JC4202
R:Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; DeWille, J.W.; Capen, C.
Gene 160, 241-243, 1995
A:Title: Sequences of the cDNAs encoding canine parathyroid hormone-related protein A
A:Reference number: JC4201; MUID:9536966
A:Accession: JC4202
A:Molecule type: mRNA
A:Residues: 1-115 <ROS>
A:Cross-references: GB:U15662; NID:g558915; PIDN:AAA82584.1; PID:g558916
C:Superfamily: parathyroid hormone; parathyroid hormone homology
C:Keywords: hormone
F:1-31/Domain: signal sequence #status Predicted <SIG>
F:30-64/Domain: parathyroid hormone homology <PTH>
F:32-115/Product: parathyroid hormone #status predicted <MAT>

Query Match 94.9%; Score 167; DB 2; Length 115;
Best Local Similarity 91.2%; Pred. No. 2.6e-14;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 XVSFIQLMHNLGKHLNSMERVWLKKLQDVHNF 34
 :|||||:|||||:|||||:|||||:|||||:|||||
Db 32 SVSFIQFMHNLGKHLSSMERVWLKKLQDVHNF 65

RESULT 5
A05091
parathyroid hormone precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Jul-1999
C:Accession: A05091; A26806
R:Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
J. Biol. Chem. 259, 3320-3329, 1984
A:Reference number: A05091; MUID:84135846
A:Accession: A05091
A:Molecule type: DNA
A:Residues: 1-115 <HEI>
A:Cross-references: GB:X01268; NID:g206483; PIDN:AAA41979.1; PID:g206485
A:Note: the authors translated the codon GAA for residue 87 as Asp
R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
Nucleic Acids Res. 15, 6740, 1987
A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid h
A:Reference number: A26806; MUID:87316938
A:Accession: A26806
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-115 <SCH>
A:Cross-references: GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA29192.1; PID:g56003
C:Genetics:
A:Introns: 29/3
C:Superfamily: parathyroid hormone; parathyroid hormone homology
F:30-64/Domain: parathyroid hormone homology <PTH>

Query Match 89.8%; Score 158; DB 2; Length 115;
Best Local Similarity 85.3%; Pred. No. 3.6e-13;
Matches 29; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 XVSFIQLMHNLGKHLNSMERVWLKKLQDVHNF 34
 :|||||:|||||:|||||:|||||:|||||:|||||
Db 32 AVSFIQLMHNLGKHLASVERMQWLKKLQDVHNF 65

RESULT 6
I51851
parathyroid hormone - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I51851
R:Schmelzer, H.
Adv. Gene Technol. 21, 228-229, 1984

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OM protein - protein search, using sw model

Run on: August 8, 2001, 16:29:17 ; Search time 10.12 seconds
(without alignments)
115.088 Million cell updates/sec

Title: US-09-447-800-1

Perfect score: 176

Sequence: 1 XVSEIQLMHNHLGKHLNLSMERVWLRKKLQDVHNF 34

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	176	100.0	115	1 PTHY_HUMAN	P01270 homo sapien
2	176	100.0	115	1 PTH_WACEA	Q9xt35 macaca fasc
3	168	95.5	115	1 PTHY_PIG	P01269 sus scrofa
4	167	94.9	115	1 PTHY_BOVIN	P01268 bos taurus
5	167	94.9	115	1 PTHY_CANFA	P52212 canis fami
6	158	89.8	115	1 PTHY_RAT	P04089 rattus norv
7	121	68.8	119	1 PTHY_CHICK	P15743 gallus gall
8	61	34.7	824	1 SYL_THEMA	Q9wy15 thermotoga
9	58	33.0	175	1 PTHR_MOUSE	P22858 mus musculu
10	58	33.0	177	1 PTHR_CANFA	P52211 canis fami
11	58	33.0	177	1 PTHR_HUMAN	P12272 homo sapien
12	58	33.0	177	1 PTHR_RAT	P13085 rattus norv
13	55	31.2	94	1 VAPD_HELPY	O05728 helicobacte
14	54	30.7	176	1 PTHR_CHICK	P17251 gallus gall
15	54	30.7	156	1 GAF2_SCHPO	Q10134 schizosacch
16	54	30.7	1257	1 RBB1_HUMAN	P29374 homo sapien
17	54	30.7	2470	1 TOR1_YEAST	P35169 saccharomyc
18	52	29.5	363	1 MURG_BORBU	O51708 borrelia bu
19	51.5	29.3	508	1 CDPK_SOYBN	P28583 glycine max
20	51.5	29.3	528	1 YJCC_ECOLI	P32701 escherichia
21	51.5	29.3	556	1 KNLK_RAT	P37285 rattus norv
22	51.5	29.3	569	1 KNLK_HUMAN	Q07866 homo sapien
23	51	29.0	611	1 HBS1_YEAST	P32769 saccharomyc
24	51	29.0	752	1 CO2_HUMAN	P06681 homo sapien
25	51	29.0	764	1 CFAB_HUMAN	P00751 homo sapien
26	51	29.0	2182	1 CAB1_RAT	O88480 rattus norv
27	51	29.0	2479	1 POLN_RRVN	P13887 ross river
28	50.5	28.7	145	1 FLIJ_BUCAI	P57179 buchera ap
29	50	28.4	89	1 VAP1_RIEAN	O85172 riemerella
30	50	28.4	91	1 VAPD_HAEIN	P71351 haemophilus
31	50	28.4	722	1 GRE4_CHLPN	Q9z794 chlamydia p
32	50	28.4	2473	1 TOR2_YEAST	P32600 saccharomyc
33	50	28.4	3678	1 DMD_MOUSE	P11531 mus musculu

RESULT	PTHY_HUMAN	1	PTHY_HUMAN	STANDARD;	PRT;	115 AA.
ID	P01270;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	13-AUG-1987 (Rel. 05, Last sequence update)					
DT	30-MAY-2000 (Rel. 39, Last annotation update)					
DE	PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH) (PARATHORMONE).					
GN	PTH.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=82150870; PubMed=6950381;					
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;					
RT	"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.";					
RL	Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=83169834; PubMed=6220408;					
RA	Vasicek T.J., McDevitt B.E., Freeman M.W., Fennick B.J.,					
RT	Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;					
RL	"Nucleotide sequence of the human parathyroid hormone gene.";					
RN	[3]					
RP	Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).					
RX	SEQUENCE OF 26-37.					
RA	MEDLINE=74174967; PubMed=4833516;					
RT	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;					
RL	"Structural analysis of human parathyroid hormone by a new microsequencing approach.";					
RN	[4]					
RP	Nature 249:155-157(1974).					
RX	SEQUENCE OF 32-68.					
RA	MEDLINE=74111656; PubMed=4521809;					
RT	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,					
RL	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;					
RT	"The amino-acid sequence of the amino-terminal 37 residues of human parathyroid hormone.";					
RL	Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).					
RN	[5]					
RP	SEQUENCE OF 61-83 AND 84-115.					
RX	MEDLINE=79082855; PubMed=728431;					
RA	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,					
RT	Potts J.T. Jr.;					
RL	"Complete amino acid sequence of human parathyroid hormone.";					
RN	[6]					
RP	SEQUENCE OF 75-100.					
RA	Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,					
RL	O'Riordan J.L.H., Potts J.T. Jr.;					
RT	(In) Talmadge R.V., Owen M., Parsons J.A. (eds.);					
RL	Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation, Amsterdam (1975).					

O46673 orcinus orc
Q09217 caenorhabdi
P09345 influenza a
P04507 reovirus (t
P33225 escherichia
Q09733 schizosacch
Q92m99 helicobacte
O25116 helicobacte
P87506 influenza a
P25348 saccharomyc
P21814 ovis aries
P16171 bacillus sp

ALIGNMENTS

hatched

[7]
REVIEWS.
RX MEDLINE=75146516; PubMed=1125201;
RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
RT "A reinvestigation of the amino-terminal sequence of human
FT parathyroid hormone";
RL Biochemistry 14:1842-1847(1975).
[8]
RX SYNTHESIS OF 32-65.
RX MEDLINE=75059220; PubMed=4474131;
RA Tregear G.W., van Rietschoten J., Green E., Niall H.D.,
RA Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
RT "Solid-phase synthesis of the biologically active N-terminal 1-34
FT peptide of human parathyroid hormone";
RL Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
[9]
RX SYNTHESIS OF 32-65.
RX MEDLINE=73227467; PubMed=4721748;
RA Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
RA Riniker B., Rittel W., Sieber P.;
RT "Synthesis of sequence 1-34 of human parathyroid hormone";
RL Helv. Chim. Acta 56:470-473(1973).
[10]
RX STRUCTURE BY NMR OF 32-65.
RX MEDLINE=91299748; PubMed=2069952;
RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;
RT "Investigation of the solution structure of the human parathyroid
FT hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,
RT and molecular dynamics calculations";
RL Biochemistry 30:6936-6942(1991).
[11]
RX STRUCTURE BY NMR OF 32-65.
RX MEDLINE=93345518; PubMed=8344299;
RA Barden J.A., Cuthbertson R.M.;
RT "Stabilized NMR structure of human parathyroid hormone(1-34).";
RL Eur. J. Biochem. 215:315-321(1993).
[12]
RX STRUCTURE BY NMR OF 32-68.
RX MEDLINE=95318084; PubMed=7797503;
RA Marx U.C., Austermann S., Bayer P., Adermann K., Eychart A.,
RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
RA Roesch P.;
RT "Structure of human parathyroid hormone 1-37 in solution.";
RL J. Biol. Chem. 270:15194-15202(1995).
[13]
RX STRUCTURE BY NMR OF 32-70.
RX MEDLINE=20090619; PubMed=10623601;
RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT "Solution structures of human parathyroid hormone fragments
FT hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
FT bPTH(1-37).";
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).
[14]
RX VARIANT ARG-18.
RX MEDLINE=91009811; PubMed=2212001;
RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
RA Kronenberg H.M.;
RT "Mutation of the signal peptide-encoding region of the
FT preproparathyroid hormone gene in familial isolated
FT hypoparathyroidism";
RL J. Clin. Invest. 86:1084-1087(1990).
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -!- DISEASE: DEFECTS IN PTH ARE A CAUSE OF FAMILIAL ISOLATED
CC HYPOPARATHYROIDISM (FIH).
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC
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CC
CC EMBL: J00301; AAA60215.1;
DR EMBL: V00597; CAA23843.1;
DR EMBL: A29146; CAA01956.1;
DR PIR: A01536; PTHU;
DR PIR: A19339; A19339;
DR PDB: 1HPH; 10-JUL-95.
DR PDB: 12WA; 12-MAR-97.
DR PDB: 12WB; 12-MAR-97.
DR PDB: 12WD; 12-MAR-97.
DR PDB: 12WE; 12-MAR-97.
DR PDB: 12WF; 16-JUN-97.
DR PDB: 12WG; 16-JUN-97.
DR PDB: 1BWX; 14-JAN-00.
DR PDB: 1HPY; 14-JAN-00.
DR MIM: 146200;
DR MIM: 168450;
DR InterPro; IPR001415;
DR Pfam: PF01279; Parathyroid; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
KW Hormone; Signal; Disease mutation; 3D-structure.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT VARIANT 18 18
FT
FT C -> R (IN FIH: LEADS TO INEFFICIENT
FT PROCESSING OF THE PRECURSOR).
FT /FTIG-VAR_006047.
FT N -> D (IN REF. 5).
SQ CONFLICT 107 107
SEQUENCE 115 AA; 12861 MW; 849015736A65597 CRC64;

Query Match 100.0%; Score 176; DB 1; Length 115;
Best Local Similarity 97.1%; Pred. No. 4.2e-16;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XVSEIOLMNLGKHLNEMERVEWLRKKLQDVHNF 34
:|||||
DB 32 SVSEIOLMNLGKHLNEMERVEWLRKKLQDVHNF 65
:

RESULT 2
PTH_MACFA STANDARD; PRT; 115 AA.
ID PTH_MACFA
AC Q9XT35;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Malaivijitnond S., Takenaka O.;
RT "Nucleotide sequences of parathyroid gene in five species of macaque
FT of Thailand";
RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC
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```
CC -----
DR EMBL; AF130257; AAD42777.1; -.
DR HSSP; P01270; IHPY.
DR InterPro; IPR001415; -.
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
DR Hormone; Signal.
KW SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 115 AA; 12890 MW; 8C2500EF24BE597 CRC64;

Query Match 100.0%; Score 176; DB 1; Length 115;
Best Local Similarity 97.1%; Pred. No. 4.2e-16;
Matches 33; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 XVSIEQLMHNIGKHLNSMERVWLKRLQDVHNF 34
DB 32 XVSIEQLMHNIGKHLNSMERVWLKRLQDVHNF 65

RESULT 3
PTHY_PIG
ID PTHY_PIG STANDARD; PRT; 115 AA.
AC P01269;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
preproparathyroid hormone from pig and rat.";
RL Nucleic Acids Res. 15:6740-6740(1987).
RN [2]
RP SEQUENCE OF 26-115.
RX MEDLINE=76018954; PubMed=1164500;
RA Chu L.H., Huang W.-Y., Littlelike E.T., Hamilton J.W., Cohn D.V.;
RT "Porcine preproparathyroid hormone. Identification, biosynthesis, and
partial amino acid sequence.";
RL Biochemistry 14:3631-3635(1975).
RN [3]
RP SEQUENCE OF 32-115.
RX MEDLINE=74253317; PubMed=4840833;
RA Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
Potts J.T. Jr.;
RT "The amino acid sequence of porcine parathyroid hormone.";
RL Biochemistry 13:1994-1999(1974).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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DR EMBL; X05722; CAA29193.1; -.
DR PIR; A01535; PTPG.
DR PIR; B26806; B26806.
DR HSSP; P01270; IHPH.
DR InterPro; IPR001415; -.

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DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
DR Hormone; Signal.
KW SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115 PARATHYROID HORMONE.
SQ SEQUENCE 115 AA; 12852 MW; 9FE8BCDE614BAC16 CRC64;

Query Match 95.5%; Score 168; DB 1; Length 115;
Best Local Similarity 91.2%; Pred. No. 4.5e-15;
Matches 31; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 XVSIEQLMHNIGKHLNSMERVWLKRLQDVHNF 34
DB 32 XVSIEQLMHNIGKHLNSMERVWLKRLQDVHNF 65

RESULT 4
PTHY_BOVIN
ID PTHY_BOVIN STANDARD; PRT; 115 AA.
AC P01268;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80056617; PubMed=388425;
RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
Potts J.T. Jr., Rich A.;
RT "Cloning and nucleotide sequence of DNA coding for bovine
preproparathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82037785; PubMed=6170060;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Introduction by molecular cloning of artifactual inverted sequences
at the 5' terminus of the sense strand of bovine parathyroid hormone
cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=83105964; PubMed=6185374;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RL Mol. Cell. Endocrinol. 28:411-424(1982).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=84262483; PubMed=6086460;
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT "Isolation and complete nucleotide sequence of the gene for bovine
parathyroid hormone.";
RL Gene 28:319-329(1984).
RN [5]
RP SEQUENCE OF 26-115.
RX MEDLINE=74142666; PubMed=4522780;
RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
Cohn D.V.;
RT "The N-terminal amino-acid sequence of bovine preproparathyroid
hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
RN [6]
RP SEQUENCE OF 32-115.
RX MEDLINE=71076162; PubMed=5531031;
RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,

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RA Aurbach G.D., Potts J.T. Jr.;
RT "The amino acid sequence of bovine parathyroid hormone I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
RN [7]
RP SEQUENCE OF 32-115
RX MEDLINE=71063634; PubMed=5275384;
RA Brewer H.B. Jr., Ronan R.;
RT "Bovine parathyroid hormone: amino acid sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
RN [8]
RP SYNTHESIS OF 32-65
RX MEDLINE=71091588; PubMed=4322265;
RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
RT Defetos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
RA "Synthesis of a biologically active N-terminal tetraoctapeptide
RT of parathyroid hormone.";
RL Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
RN [9]
RP STRUCTURE BY NMR OF 32-68.
RX MEDLINE=20090619; PubMed=10623601;
RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
RT "Solution structures of human parathyroid hormone fragments
RT hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
RT bPTH(1-37).";
RL Biochem. Biophys. Res. Commun. 267:213-220(2000).
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL; V00106; CAA23439.1; -
DR EMBL; J00024; AAA30747.1; -
DR EMBL; K01938; AAA30749.1; -
DR EMBL; M25082; AAA30748.1; -
DR PIR; A01534; PTBO.
DR PIR; A24949; A24949.
DR PDB; 1ZWC; 12-MAR-97.
DR InterPro; IPR001415; -
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal; 1 25
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT SEQUENCE 115 AA; 12980 MW; 2ED246B348880710 CRC64;
CC -----
Query Match 94.9%; Score 167; DB 1; Length 115;
Best Local Similarity 91.2%; Pred. No. 6.1e-15;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 XVSEIQLMHNKGLHLSMERVEWLKKLQDVHNF 34
Db 32 AVSEIQLMHNKGLHLSMERVEWLKKLQDVHNF 65
:||||| |||||||:|||||
RESULT 5
PTHY_CANFA
ID PTHY_CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.

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OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Parathyroid;
RX MEDLINE=95369696; PubMed=7642102;
RA Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A.,
RA DeWille J.W., Capen C.C.;
RT "Sequences of the cDNAs encoding canine parathyroid hormone-related
RT protein and parathyroid hormone.";
RL Gene 160:241-243(1995).
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
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CC -----
DR EMBL; U15662; AAA82584.1; -
DR HSSP; P01270; 1ZWC.
DR InterPro; IPR001415; -
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;
CC -----
Query Match 94.9%; Score 167; DB 1; Length 115;
Best Local Similarity 91.2%; Pred. No. 6.1e-15;
Matches 31; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 XVSEIQLMHNKGLHLSMERVEWLKKLQDVHNF 34
Db 32 SVSEIQLMHNKGLHLSMERVEWLKKLQDVHNF 65
:||||| |||||||:|||||
RESULT 6
PTHY_RAT
ID PTHY_RAT STANDARD; PRT; 115 AA.
AC P04089; Q63473;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PARATHYROID HORMONE PRECURSOR (PARATHYRIN) (PTH).
GN PTH.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84135846; PubMed=6321505;
RA Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
RT "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
RT gene and deduced amino acid sequence of rat preproparathyroid
RT hormone.";
RL J. Biol. Chem. 259:3320-3329(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87316938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
RT preproparathyroid hormone from pig and rat.";

```

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OM protein - protein search, using sw model

Run on: August 8, 2001, 16:29:17 ; Search time 21.09 Seconds
(without alignments)
213.294 Million cell updates/sec

Title: US-09-447-800-1
Perfect score: 176
Sequence: 1 XVSQTLMHNLGKHLNSMERVWLKKLQDVHNF 34

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172	97.7	86	Q9N1V0	Q9N1V0 equus caball
2	160	90.9	115	Q9GL67	Q9GL67 felis silve
3	156	88.6	115	Q9Z0L6	Q9Z0L6 mus musculus
4	78	44.3	163	Q918E9	Q918E9 fugu rubrip
5	75	42.6	162	Q918U2	Q918U2 sparus aura
6	58	33.0	121	Q9GK30	Q9GK30 ovis aries
7	58	33.0	177	Q9GLC7	Q9GLC7 oryctolagus
8	56	31.8	115	Q9YD49	Q9YD49 aeropyrum p
9	54	30.7	851	Q15993	Q15993 homo sapien
10	54	30.7	866	Q15992	Q15992 homo sapien
11	54	30.7	920	Q15991	Q15991 homo sapien
12	53.5	30.4	130	Q70327	Q70327 mesocricetu
13	53	30.1	787	Q9V5M8	Q9V5M8 drosophila
14	52.5	29.8	303	Q9VIA4	Q9VIA4 drosophila
15	52.5	29.8	711	Q24164	Q24164 drosophila
16	52.5	29.8	785	Q9NBK6	Q9NBK6 drosophila
17	52	29.5	787	Q9VCX5	Q9VCX5 drosophila
18	51.5	29.3	153	Q99786	Q99786 homo sapien
19	51.5	29.3	487	Q90707	Q90707 gallus gall

20	51.5	29.3	541	11	O88447	O88447 mus musculus
21	51.5	29.3	548	14	P88828	P88828 influenza a
22	51.5	29.3	548	14	P88834	P88834 influenza a
23	51.5	29.3	651	5	Q9N8V3	Q9N8V3 trypanosoma
24	51.5	29.3	872	4	Q9H3R1	Q9H3R1 homo sapien
25	51.5	29.3	872	11	Q9E0W8	Q9E0W8 mus musculus
26	51.5	29.3	873	4	O95803	O95803 homo sapien
27	51.5	29.3	873	11	Q9EQH7	Q9EQH7 mus musculus
28	51.5	29.3	876	4	Q9UP21	Q9UP21 homo sapien
29	51	29.0	336	2	Q9K7V5	Q9K7V5 bacillus ha
30	51	29.0	386	3	P79004	P79004 saccharomyc
31	51	29.0	977	5	Q9U0H9	Q9U0H9 plasmodium
32	51	29.0	1038	5	O61199	O61199 caenorhabdi
33	51	29.0	1500	5	Q9VLQ8	Q9VLQ8 drosophila
34	50.5	28.7	3394	5	O77384	O77384 plasmodium
35	50	28.4	96	2	Q9RQR1	Q9RQR1 riemerella
36	50	28.4	180	4	Q9H4V3	Q9H4V3 homo sapien
37	50	28.4	279	4	Q9NW78	Q9NW78 homo sapien
38	50	28.4	415	4	Q9H4V2	Q9H4V2 homo sapien
39	50	28.4	561	5	Q9N341	Q9N341 caenorhabdi
40	50	28.4	570	1	Q9YCM6	Q9YCM6 aeropyrum p
41	50	28.4	590	11	Q9ERD6	Q9ERD6 mus musculus
42	49.5	28.1	264	13	Q9PS76	Q9PS76 gallus gall
43	49.5	28.1	292	13	Q9PS77	Q9PS77 gallus gall
44	49.5	28.1	339	5	Q17633	Q17633 caenorhabdi
45	49.5	28.1	490	10	Q42396	Q42396 arabidopsis

ALIGNMENTS

RESULT 1
Q9N1V0 PRELIMINARY; PRT; 86 AA.
AC Q9N1V0:
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE PARATHYROID HORMONE (FRAGMENT).
GN PTH.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=10613847;
RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249(1999).
DR EMBL; AF134233; AAF62347.1; -;
DR InterPro; IPR001415; -;
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1
SQ SEQUENCE 86 AA; 9805 MW; 253184EA681A2022 CRC64;

Query Match 97.7%; Score 172; DB 6; Length 86;
Best Local Similarity 94.1%; Pred. No. 9.6e-15;
Matches 32; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 XVSQTLMHNLGKHLNSMERVWLKKLQDVHNF 34
:|||||
Db 3 SVSQTLMHNLGKHLNSMERVWLKKLQDVHNF 36

RESULT 2
Q9GL67 PRELIMINARY; PRT; 115 AA.
ID Q9GL67:
AC Q9GL67:
DT 01-MAR-2001 (TRENBLrel. 16, Created)

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DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE PREPROPARATHYROID HORMONE PRECURSOR.
GN PTH.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
RT "Molecular cloning of feline preproparathyroid hormone.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309967; AAC30545.1; -.
KW Signal.
FT SIGNAL.
FT CHAIN
SQ SEQUENCE 115 AA; 12921 MW; 80CD557CC6A1A47E CRC64;

Query Match 90.9%; Score 160; DB 6; Length 115;
Best Local Similarity 85.3%; Pred. No. 4.3e-13;
Matches 29; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XVSIEQLMHNIGKHLNSMERVEWLKKLQDVHNF 34
Db 32 SVSIEQFMHNIGKHLSSVERVEWLKKLQDVHNF 65

RESULT 3
Q920L6 PRELIMINARY; PRT; 115 AA.
AC Q920L6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE PARATHYROID HORMONE PRECURSOR.
GN PTH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=129/SV;
RA Karaplis A.C., He B., Hion-Tin F.F.T., Al-Akad B., Kronenberg H.M.;
RT "Cloning of the murine gene encoding parathyroid hormone: genomic
organization and nucleotide sequence.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF066075; AAC99656.1; -.
DR HSSP; P01270; 12WB.
DR InterPro; IPR001415; -.
DR InterPro; IPR003625; -.
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
DR SMART; SM00087; PTH; 1.
KW Signal.
FT SIGNAL.
FT CHAIN
SQ SEQUENCE 115 AA; 12825 MW; DA43FABBCB4E2FD9 CRC64;

Query Match 88.6%; Score 156; DB 11; Length 115;
Best Local Similarity 82.4%; Pred. No. 1.4e-12;
Matches 28; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 XVSIEQLMHNIGKHLNSMERVEWLKKLQDVHNF 34
Db 32 AVSIEQLMHNIGKHLASMERQWLKKLQDMHNF 65

RESULT 4
Q918E9 PRELIMINARY; PRT; 163 AA.
AC Q918E9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR.
GN PTHRP.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20314478; PubMed=10854780;
RA Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,
RA Elgar G., Clark M.S.;
RT "Genomic structure and expression of parathyroid hormone-related
protein in a teleost, Fugu rubripes.";
RL Gene 250:67-79(2000).
DR EMBL; AJ249391; CAB94712.1; -.
DR InterPro; IPR001415; -.
DR Pfam; PF01279; Parathyroid; 1.
KW Signal.
FT SIGNAL.
FT CHAIN
SQ SEQUENCE 163 AA; 18698 MW; 3AC5F2C764732278 CRC64;

Query Match 44.3%; Score 78; DB 13; Length 163;
Best Local Similarity 46.9%; Pred. No. 0.015;
Matches 15; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 1 XVSIEQLMHNIGKHLNSMERVEWLKKLQDVH 32
Db 38 SVSHAQLMHDKGRSLQEFRRRMWLKLEEVH 69

RESULT 5
Q918U2 PRELIMINARY; PRT; 162 AA.
AC Q918U2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PARATHYROID HORMONE-RELATED PROTEIN PRECURSOR.
GN PTHLH.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=KIDNEY;
RA MEDLINE=20304721; PubMed=10843788;
RA Flanagan J.A., Power D.M., Bendall L.A., Guerreiro P.M., Fuentes J.,
RA Clark M.S., Canario A.V.M., Danks J.A., Brown B.L., Ingleton P.M.;
RT "Cloning of the cDNA for sea bream (Sparus aurata) Parathyroid
hormone-related protein.";
RL Gen. Comp. Endocrinol. 118:373-382(2000).
DR EMBL; AF197904; AAF79073.1; -.
DR InterPro; IPR001415; -.
DR InterPro; IPR003571; -.
DR Pfam; PF01279; Parathyroid; 1.
DR PROSITE; PS00206; -.
DR SEQUENCE 162 AA; 18722 MW; 6E8D5E07F9E5EDC9 CRC64;

Query Match 42.6%; Score 75; DB 13; Length 162;
Best Local Similarity 43.8%; Pred. No. 0.036;

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Qy 1 X V S E I Q L M H N L G K H L N S M E R V E W L R K K L Q D V H 32
 : : : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 37 AVSEHQLLHDKGKSIODLRRRRFFLLHLIAEIH 68

Best Local Similarity 38.1%; Pred. No. 94;
Matches 8: Conservative 9: Mismatches 4: Indels

Qy 1 X V S E I Q L M H N L G K H L N S M E R V E W L R K K L Q D V H 32
 : : : : | | : : | | : : | | : : | | : : | | : : | | : : | |
Db 37 A V S E H Q L L H D K G K S I O D L R R R F F L H H L I A E I H 68

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Qy 14 HLNSMERVEWLKRLQDVHNF 34
Db 773 NMNSTERISFLOEKLOEIRKY 793

RESULT 10
Q15992
AC Q15992; PRELIMINARY; PRT; 866 AA.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE RETINOBLASTOMA BINDING PROTEIN I ISOFORM II (FRAGMENT).
GN RBP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93205410; PubMed=8455946;
RA Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
RT "Alternative splicing of the RBP1 gene clusters in an internal exon
RL Oncogene 8:949-957(1993).
DR EMBL; S57160; AAB25834.1; -
DR InterPro; IPR000953; -
DR InterPro; IPR001606; -
DR Pfam; PF01388; ARID.1; -
DR SMART; SM00298; CHROMO; 1.
FT NON_TER 1
SQ SEQUENCE 866 AA; 98332 MW; 2DCFA7A8CE06B125 CRC64;

Query Match 30.7%; Score 54; DB 4; Length 866;
Best Local Similarity 38.1%; Pred. NO. 95;
Matches 8; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 14 HLNSMERVEWLKRLQDVHNF 34
Db 788 NMNSTERISFLOEKLOEIRKY 808

RESULT 11
Q15991
AC Q15991; PRELIMINARY; PRT; 920 AA.
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE RETINOBLASTOMA BINDING PROTEIN I ISOFORM I (FRAGMENT).
GN RBP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93205410; PubMed=8455946;
RA Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
RT "Alternative splicing of the RBP1 gene clusters in an internal exon
RL Oncogene 8:949-957(1993).
DR EMBL; S57153; AAB25833.1; -
DR InterPro; IPR001606; -
DR Pfam; PF01388; ARID.1; -
DR SMART; SM00501; BRIGHT; 1.
FT NON_TER 1
SQ SEQUENCE 920 AA; 104589 MW; BD37B5F59009570A CRC64;

Query Match 30.7%; Score 54; DB 4; Length 920;

Best Local Similarity 38.1%; Pred. NO. 1e+02;
Matches 8; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 14 HLNSMERVEWLKRLQDVHNF 34
Db 842 NMNSTERISFLOEKLOEIRKY 862

RESULT 12
Q15992
AC Q15992; PRELIMINARY; PRT; 130 AA.
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE INTERLEUKIN-10 (FRAGMENT).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=SPLEEN;
RX MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis."
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046210; AAC40095.1; -
DR HSP; P22301; IINR.
DR InterPro; IPR000098; -
DR Pfam; PF00726; IL10; 1.
DR PRINTS; PR01294; INTRLEUKIN10.
DR PROSITE; PS00520; INTERLEUKIN_10; 1.
DR SMART; SM00188; IL10; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15260 MW; DAFE3B5FC216B380 CRC64;

Query Match 30.4%; Score 53.5; DB 11; Length 130;
Best Local Similarity 47.8%; Pred. NO. 15;
Matches 11; Conservative 7; Mismatches 4; Indels 1; Gaps 1;

Qy 13 KHLNSM-ERVEWLKRLQDVHNF 34
Db 74 EHLNSLGEKLTLLRQLQCHRF 96

RESULT 13
Q15958
AC Q15958; PRELIMINARY; PRT; 787 AA.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE LOLA PROTEIN (BTB-IV PROTEIN DOMAIN).
OS LOLA OR BTBIV OR CG12052 OR CG18376.
OC Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbavani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE OF 5-119 FROM N.A.
 RX MEDLINE=95024186; PubMed=7938017;
 RA Zollman S., Godt D., Prive G.G., Couderc J.L., Laski F.A.;
 RA "The BTB domain, found primarily in zinc finger proteins, defines an
 RT evolutionarily conserved family that includes several developmentally
 RT regulated genes in Drosophila.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:10717-10721(1994).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 DR EMBL; AE003829; AAF58774.1; -;
 DR EMBL; AE003829; AAF58777.1; -;
 DR EMBL; U14401; AAA50836.1; -;
 DR Flybase; FBgn005630; lola.
 DR InterPro; IPR000210; -;
 DR Pfam; PF00096; zf-C2H2; 2.
 DR Pfam; PF00651; BTB; 1.
 DR PROSITE; PS0097; BTB; 1.
 KW Alternative splicing.
 FT VARSPLIC 455
 FT DLSITRIAGLT -> GECLLPKSI (IN SHORT
 FT ISOFORM).
 FT VARSPLIC 466 787
 FT MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 787 AA; 82173 MW; 6P20570E6C1A4702 CRC64;

Query Match 30.1%; Score 53; DB 5; Length 787;
 Best Local Similarity 48.3%; Pred. No. 1.2e+02;

Matches 14; Conservative 5; Mismatches 6; Indels 4; Gaps 2;

Qy 6 QLMHNLGKHLNSMERVWLRKKLQDVHNF 34
 | | | | | : | | | : | | | | |
 Db 725 QKMH-IGRH---MERHKEKPKLEDVKNF 749

RESULT 14
 Q9VIA4
 ID Q9VIA4 PRELIMINARY; PRT; 303 AA.
 AC Q9VIA4;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2001 (TREMBLrel. 16, Last annotation update)
 DE MSTPROX PROTEIN.
 GN MSTPROX OR CG1149.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BERKELEY.
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbavani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 RL EMBL; AE003672; AAF54021.1; -;
 DR Flybase; FBgn0015770; Matprox.
 DR InterPro; IPR000372; -;
 DR Pfam; PF01462; LRRTNT; 1.
 DR SMART; SM00013; LRRTNT; 1.
 SQ SEQUENCE 303 AA; 35689 MW; 57BA402F6AF764D5 CRC64;

Query Match 29.8%; Score 52.5; DB 5; Length 303;
 Best Local Similarity 28.6%; Pred. No. 49;

Matches 10; Conservative 11; Mismatches 7; Indels 7; Gaps 1;

Qy 1 XVSEIQLMHNLGKHLNSMERV-----EWLRKKL 28
 : : : | | | : : | | : : | | : | |
 Db 212 LINEQLQSMHRLKLNLTNTMSIYKVMWLRKKL 246

RESULT 15
 Q24164
 ID Q24164 PRELIMINARY; PRT; 711 AA.
 AC Q24164;

Search completed: August 8, 2001, 16:31:09
Job time: 112 sec